STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/518,174_

Source: _Pct/ip_

Date Processed by STIC: _5/3/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio. (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/518,174_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ____ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)　　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 ____ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 ____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

PCT

```
      5 <110> APPLICANT: Aston University
      7 <120> TITLE OF INVENTION: Methods of Producing DNA and Protein Libraries
      9 <130> FILE REFERENCE: W071488PPC
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/518,174
C--> 12 <141> CURRENT FILING DATE: 2004-12-13
     14 <150> PRIOR APPLICATION NUMBER: GB0213816.2
     15 <151> PRIOR FILING DATE: 2002-06-14
     17 <160> NUMBER OF SEQ ID NOS: 13
     19 <170> SOFTWARE: PatentIn version 3.1
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 52
     23 <212> TYPE: DNA
     24 <213> ORGANISM: Artificial sequence
     26 <220> FEATURE:
     27 <223> OTHER INFORMATION: consensus zinc finger gene fragment
     28 <220> FEATURE:
     29 <221> NAME/KEY: misc_feature
     30 <222> LOCATION: (16)..(18)
     31 <223> OTHER INFORMATION: n=site of randomisation
     32 <220> FEATURE:
     33 <221> NAME/KEY: misc_feature
     34 <222> LOCATION: (25)..(27)
     35 <223> OTHER INFORMATION: n=site of randomisation
     37 <220> FEATURE:
     38 <221> NAME/KEY: misc_feature
     39 <222> LOCATION: (34)..(36)
     40 <223> OTHER INFORMATION: n=site of randomisation
     41 <400> SEQUENCE: 1
W--> 42   ctgacttcga aatcannntc gctgnnnaat gttnnngtag tcgcatgctg ca          52
     43 <210> SEQ ID NO: 2
     44 <211> LENGTH: 15
     45 <212> TYPE: DNA
     46 <213> ORGANISM: Artificial sequence
     48 <220> FEATURE:
     49 <223> OTHER INFORMATION: PCR primer
     50 <400> SEQUENCE: 2
     51  gactgaagct ttagt                                                     15
     52 <210> SEQ ID NO: 3
     53 <211> LENGTH: 16
     54 <212> TYPE: DNA
     55 <213> ORGANISM: Artificial Sequence
     57 <220> FEATURE:
     58 <223> OTHER INFORMATION: PCR primer
```

pp 1-5

Does Not Comply
Corrected Diskette Needed

please explain n's further — which nucleotides would they represent?

RAW SEQUENCE LISTING   DATE: 03/03/2006
PATENT APPLICATION: **US/10/518,174**   TIME: 12:49:08

Input Set : **N:\DA\pto.da.txt**
Output Set: **N:\CRF4\03032006\J518174.raw**

```
 59 <400> SEQUENCE: 3
 60   gtcgctggtc tactac                                              16
 62 <210> SEQ ID NO: 4
 63 <211> LENGTH: 18
 64 <212> TYPE: DNA
 65 <213> ORGANISM: Artificial Sequence
 67 <220> FEATURE:
 68 <223> OTHER INFORMATION: partial complementary sequence to SEQ ID 1
 69 <220> FEATURE:
 70 <221> NAME/KEY: misc_feature
 71 <222> LOCATION: (16)..(18)
 72 <223> OTHER INFORMATION: nnn represents MAX codon (optimum codon usage for each amino
                   acid
 73          in E. coli)
 75 <400> SEQUENCE: 4
W--> 76   gactgaagct ttagtnnn                                         18
 78 <210> SEQ ID NO: 5
 79 <211> LENGTH: 32
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Artificial Sequence
 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: complementary sequence to SEQ ID 3 and SEQ ID 6 (partially)
 85 <400> SEQUENCE: 5
 86   catcagcgta cgacgtcagc gaccagatga tg                            32
 87 <210> SEQ ID NO: 6
 88 <211> LENGTH: 42
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Artificial Sequence
 92 <220> FEATURE:
 93 <223> OTHER INFORMATION: consensus zinc finger gene fragment
 94 <220> FEATURE:
 95 <221> NAME/KEY: misc_feature
 96 <222> LOCATION: (6)..(8)
 97 <223> OTHER INFORMATION: n=site of randomisation
 99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (15)..(17)
102 <223> OTHER INFORMATION: n=site of randomisation
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (24)..(26)
107 <223> OTHER INFORMATION: n=site of randomisation
109 <400> SEQUENCE: 6
W--> 110   aatcannntc gctgnnnaat gttnnngtag tcgcatgctg ca               42
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 15
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: PCR primer
```

[handwritten annotations:] Shorter line - see item 2 on Euro summary sheet

have over

see item 2 on Euro summary sheet

```
119 <400> SEQUENCE: 7
120  atgaccatga ttacg                                                    15
122 <210> SEQ ID NO: 8
123 <211> LENGTH: 30
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence          all Item 2
127 <220> FEATURE:
128 <223> OTHER INFORMATION: complementary sequence to SEQ ID 7 and SEQ ID 1 (partially)
129 <400> SEQUENCE: 8
130  atgaccatga ttacgctatg ccatgactga                                    30
132 <210> SEQ ID NO: 9
133 <211> LENGTH: 12
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
139 <223> OTHER INFORMATION: partial complementary sequence to SEQ ID 1
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature            Item 2
143 <222> LOCATION: (10)..(12)
144 <223> OTHER INFORMATION: nnn represents MAX codon (optimum codon usage for each amino
acid        move over
145                  in E. coli)
148 <400> SEQUENCE: 9.
149  agctttagtn nn                                                       12
151 <210> SEQ ID NO: 10
152 <211> LENGTH: 15
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: PCR primer
158 <400> SEQUENCE: 10
159  acttgagact gaagc                                                    15
161 <210> SEQ ID NO: 11
162 <211> LENGTH: 15
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: PCR primer
168 <400> SEQUENCE: 11
169  gcatgctaga ctgcc                                                    15
171 <210> SEQ ID NO: 12
172 <211> LENGTH: 21
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: complementary sequence to SEQ ID 11 and SEQ ID 13
(partially).        move over
178 <400> SEQUENCE: 12
179  catcagcgta cgatctgacg c                                             21
182 <210> SEQ ID NO: 13
183 <211> LENGTH: 39
```

W--> 149 agctttagtn nn   (handwritten annotation)

```
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: consensus zinc finger gene fragment
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (13)..(15)
192 <223> OTHER INFORMATION: n=site of randomisation
194 <220> FEATURE:
195 <221> NAME/KEY: misc_feature
196 <222> LOCATION: (22)..(24)
197 <223> OTHER INFORMATION: n=site of randomisation
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (31)..(34)
202 <223> OTHER INFORMATION: n=site of randomisation
204 <400> SEQUENCE: 13
```

W--> 205 acttcgaaat cannntcgct gnnaatgtt nnngtagtc   39
W--> 206 25567341.1 - 5

(handwritten annotations: "(33)", "g is at location 4", "delete")

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/03/2006
PATENT APPLICATION: US/10/518,174   TIME: 12:49:09

Input Set : **N:\DA\pto.da.txt**
Output Set: **N:\CRF4\03032006\J518174.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 16,17,18,25,26,27,34,35,36
Seq#:4; N Pos. 16,17,18
Seq#:6; N Pos. 6,7,8,15,16,17,24,25,26
Seq#:9; N Pos. 10,11,12
Seq#:13; N Pos. 13,14,15,22,23,24,31,32,33

VERIFICATION SUMMARY   DATE: 03/03/2006
PATENT APPLICATION: **US/10/518,174**   TIME: 12:49:09

Input Set : **N:\DA\pto.da.txt**
Output Set: **N:\CRF4\03032006\J518174.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:206 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4